AMD Projects

Innovate • Transform • Protect

CDC's Advanced Molecular Detection (AMD) initiative fosters scientific innovation in genomic sequencing, epidemiology, and bioinformatics to transform public health and protect people from disease threats.

AMD Projects: Analyzing Emerging Epidemics

Whole genome sequencing to assess epidemic potential of emerging meningococcal strains and monitor changes in vaccine immunogen and virulence-related genes

Meningococcal disease (meningitis, bloodstream infections) kills one out of every 10 people who get it, often within hours or days, even when antibiotics are started early. People who survive can have permanent disabilities like paralysis, hearing loss, seizures, or loss of limb(s). Meningococcal disease, which is caused by the bacteria *Neisseria meningitidis,* threatens the lives of millions of people across the meningitis belt of sub-Saharan Africa—a 26 country area stretching from Senegal in the west to Ethiopia in the east.

A vaccine (MenAfriVac™) was introduced in the meningitis belt in 2010 to prevent Africa's most common strain of *N. meningitidis*—serogroup A. Along with the vaccine's documented success at preventing illness comes many questions and challenges. For instance, will other strains circulating in the region (serogroups X and W) start causing

More than 217 million eligible Africans in 15 countries were vaccinated with MenAfriVac™ by 2015.

www.cdc.gov/amd

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more disease now that there is less serogroup A in these countries? How dangerous are those strains? Are they genetically linked to other strains? And most importantly, are available vaccines effective against these other strains?

To answer these questions, CDC's laboratory scientists are using whole genome sequencing (WGS) to analyze hundreds of meningococcal isolates (bacteria grown from clinical samples) from the meningitis belt. Researchers are comparing these isolates to strains causing sporadic disease and outbreaks worldwide. Using new laboratory tools, CDC will be able to compare how closely related the strains are and find markers for how likely they are to cause epidemics.

Using WGS analysis, meningitis experts will be better at predicting meningococcal disease epidemics at an early stage and know if available vaccines are effective against these strains. This vital information will help Ministries of Health and policy makers in structuring vaccination decisions and improving public health response.

For more information on meningococcal disease, please visit the CDC website, www.cdc.gov/meningococcal/about/index.html.

2016 Update

In the first year, CDC researchers completed WGS on isolates from before and after MenAfriVac™ introduction, examining the three most common strains of *N. meningitidis* in the region. While these isolates are being analyzed, researchers will continue to sequence isolates from surveillance systems and evaluate the impact of MenAfriVac™ on circulating strains. Since many laboratories in the meningitis belt do not have the capacity to conduct this type of analysis, researchers are working to create new tools these laboratories can use to quickly identify meningococcal strains with epidemic potential. Finally, researchers are creating an online library for comparing the meningococcal genomes with reference strains. This library will help laboratory scientists from across the world track the strains of *N. meningitidis* that are circulating globally.

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